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RESEARCH ARTICLE

Deciphering genetic variation in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] through multivariate analysis

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Abstract

This study evaluated genetic variability, trait associations, and multivariate divergence among fifty horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] genotypes using an Augmented Block Design with six checks replicated across three blocks. Data on eight quantitative traits, including seed yield, were analysed through standard statistical methods. Significant variability was observed across all traits, indicating ample scope for selection and improvement. High genotypic and phenotypic coefficients of variation, coupled with high heritability and genetic advance for seed yield and number of pods per plant, emphasized their importance as primary selection criteria. Correlation analysis revealed that seed yield was positively and significantly associated with pods per plant, seeds per pod, days to flowering, and days to maturity, highlighting the role of these traits in yield enhancement. Principal component analysis (PCA) demonstrated that the first two components accounted for more than 62% of the total variation, with PC1 reflecting yield and maturity traits, while PC2 represented seed size and branching. Biplot analysis effectively identified promising genotypes with superior yield attributes and clarified interrelationships among traits. Overall, the study confirmed substantial genetic diversity in horse gram germplasm and identified promising lines with potential for use in breeding programs aimed at yield improvement and adaptability.

Keywords: Horsegram, genetic variability, correlation, principal component analysis (PCA)

Introduction

Horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.), a member of the family Fabaceae, is a hardy, drought-resistant legume that remains largely underutilized despite its significant agronomic, nutritional, and medicinal potential. It is predominantly cultivated in the tropical and subtropical regions of Asia and Africa, where it serves as a dual-purpose crop-supporting both human nutrition and livestock feed systems (Bhartiya et al. 2015). Among these regions, India stands as the largest producer, with approximately 5.07 lakh hectares under cultivation and a production volume of 2.62 lakh tonnes, translating to an average productivity of 516 kg ha^{-1} (Ain and Ain 2024). Despite these figures, the productivity of horse gram remains low, primarily due to minimal investment in its genetic improvement and a lack of systematic research focus.

Locally, horse gram is known by various vernacular names-*Kulattha*, *Kurti-kalai*, *Kollu*, *Ullavallu*, *Muthira*, and *Gahot*reflecting its deep cultural and ethnobotanical significance. The term *Gahot*, for instance, is derived from its traditional use in treating kidney stones, meaning «that which destroys stone in the initial stage» (Pati and Bhattacharjee 2013). The crop is not only valued for its ethnomedicinal properties but also for its nutritional profile, being rich in protein, dietary fiber, iron, calcium, and polyphenols, making it an important functional food in many indigenous diets.

Morphologically, horse gram is a photo- and thermo-sensitive, short-day annual herbaceous climber characterized

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by its trifoliate leaves, small white flowers, long linear pubescent pods with a distinctively curved beak, and small seeds exhibiting a range of testacolors including red, brown, grey, black, and mottled forms (Singh 1991; Kumar 2006). Its ability to grow on marginal soils under rainfed, low-input conditions makes it particularly well-suited for cultivation in arid and semi-arid agro-climatic regions. This resilience positions horse gram as a sustainable crop of future importance, particularly in the context of climate change and food security in resource-poor areas.

However, despite its various advantages, horse gram remains neglected in mainstream agricultural research and crop improvement programs. Unlike other major pulses such as chickpea, pigeon pea, or mung bean, horse gram has received minimal attention in terms of systematic evaluation, genetic characterization, and breeding efforts. This neglect has led to stagnation in yield and limited progress in developing improved varieties with desirable traits.

Nevertheless, existing research indicates that the horse gram germplasm harbors substantial genetic diversity, which, if properly characterized and utilized, can serve as a valuable reservoir for breeding programs aimed at yield improvement and stress tolerance. Several studies have emphasized the significance of germplasm evaluation and trait-based selection strategies in identifying superior genotypes for use as parents in breeding programs (Vijayakumar et al. 2016; Bhavsar et al. 2021; Priyanka et al. 2021a). Furthermore, the application of statistical tools such as correlation analysis, path coefficient analysis, and multivariate techniques like principal component analysis (PCA) and cluster analysis has been advocated for dissecting complex traits and elucidating the genetic relationships among genotypes (Bhardwaj and Yadav 2020).

In this context, a clear understanding of genetic variability, trait interrelationships, and diversity patterns among horse gram genotypes is fundamental for designing effective breeding strategies and for selecting appropriate parental materials in crop improvement programmes. Such information enables researchers to characterize the available germplasm more precisely and to plan hybridization efforts based on complementary traits and genetic divergence. Therefore, the present study was undertaken with the specific objectives of assessing the extent of genetic variability among fifty horse gram genotypes, along with examining the interrelationships among important quantitative traits through correlation analysis and determining the pattern of multivariate divergence using principal component analysis. These objectives were framed to generate essential primary information required for strengthening future breeding initiatives in horse gram.

Materials and methods

The present study was conducted during the *kharif* 2019 & 2020 at Dr. B. R. Choudhary Agricultural Research Station, Mandor, under Agriculture University, Jodhpur, to evaluate 50 genotypes of horse gram for genetic variability, trait associations, and multivariate divergence. The experiment was carried out in an Augmented Block Design (ABD), which is effective for evaluating a large number of genotypes with check replication. The 50 genotypes were distributed across three blocks, with Block I and Block II comprising 17 genotypes each and Block III comprising 16 genotypes. The list of genotypes is given in

Table 1. Six check varieties were included in each block to facilitate inter-block comparisons and improve the accuracy of selection.

Each genotype was sown in a plot consisting of five rows, every 4 meters in length, with a spacing of 45 cm between rows and 15 cm between plants. Standard agronomic practices were uniformly followed throughout the experiment to ensure optimal plant growth and to minimize environmental variation. Data were recorded on eight quantitative traits from five randomly selected competitive plants per genotype. These traits included days to 50% flowering, days to maturity, number of primary branches per plant, plant height (cm), number of pods per plant, number of seeds per pod, 1000 seed weight (g), and seed yield (kg/ha).

Statistical analysis was performed with pooled data of these two years using software GRAPES 1.1.0 (General R-based Analysis Platform Empowered by Statistics), developed by Gopinath et al. (2020). Adjusted means were computed based on the principles of augmented block design. Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated following Burton and Devane (1953), while heritability (broad sense), genetic advance (GA), and genetic advance as percent of mean (GAM) were estimated using the methods outlined by Johnson et al. (1955), Al-Jibouri et al. (1958), and Dewey and Lu (1959). Pearson's correlation coefficients were computed to study the interrelationships among traits. Principal Component Analysis (PCA) was used to identify the traits contributing most to genetic variability. A scree plot was generated to determine the number of significant components based on eigenvalues, and a biplot was constructed to visualize the distribution of genotypes and the association among traits.

Results

The analysis of variance (ANOVA) revealed highly significant differences among the genotypes for all traits studied, indicating the presence of substantial genetic variability within the tested genotypes (Tables 2 and 3).

Genetic variability

The adjusted mean values for seed yield and key yield-contributing traits across 50 horse gram genotypes are presented in Table 4. The analysis of variance (ANOVA) among fifty horse gram genotypes for eight quantitative

Table 1. List of genotypes evaluated in the study, which were collected from different institutes and derived from diverse genetic backgrounds

S. No.	Name of genotype	Centre/Institute Name	Pedigree/Source Population
1.	VL Gahat-8	VIPKAS, Almora	VLG-1 X P-1648-1
2.	VL Gahat-10	VIPKAS, Almora	VLG-1 X NIC-2659
3.	VL Gahat-15	VIPKAS, Almora	VLG-2 X NIC-2659-2
4.	VL Gahat-19	VIPKAS, Almora	Selection from VH-61
5.	VL Gahat-37	VIPKAS, Almora	VLG-10 X VRPH-264
6.	VL Gahat-38	VIPKAS, Almora	VLG-10 X VRPH-2224
7.	VLGahat-39	VIPKAS, Almora	VLG-10 X VLG-20-32
8.	BhilangnaLoca-HIMALA	VIPKAS, Almora	Selection from local germplasm
9.	AK-21	PDKV, Akola, Maharashtra	Selection from locally adapted variety of village karoi district Bhilwara, Rajasthan
10.	AK-52	PDKV, Akola, Maharashtra	
11.	Maru Kulthi	CAZRI, Jodhpur, Rajasthan	Selection from local germplasm from Pali-Marwar region
12.	BGHG-1	Unknown	
13.	BHG-13-2	Unknown	
14.	PHG 9	UAS, Bengaluru, Karnataka	
15.	CRHG-2	ICAR-CRIDA, Hyderabad	
16.	CRHG-4 (CRIDALATHA)	ICAR-CRIDA, Hyderabad	A derivative from Hyderabad local, evolved by physically induced mutation through gamma rays
17.	CRHG-8	ICAR-CRIDA, Hyderabad	
18.	CRHG-19 (CRIDAHARSHA)	ICAR-CRIDA, Hyderabad	A derivative from AK-42 evolved by physically induced mutation through gamma rays
19.	CRHG-22	ICAR-CRIDA, Hyderabad	
20.	CRHG-23	ICAR-CRIDA, Hyderabad	
21.	HG-62	Unknown	
22.	BGM 1	UAS, Bengaluru, Karnataka	
23.	PH-01-20	Unknown	
24.	IC-282587	ICAR-NBPGR, New Delhi (Paseripat/Mahuatand, Palamau, Jharkhand)	Landrace
25.	IC-283434	ICAR-NBPGR, New Delhi (Shashibhusan gram/Mohanpur, Deoghar, Jharkhand)	Selection from local germplasm
26.	IC-312383	ICAR-NBPGR, New Delhi (Tanka/Patamda, East Singhbhum, Jharkhand)	Selection from local germplasm
27.	IC-312384	ICAR-NBPGR, New Delhi (Huludbani/Patamda, East Singhbhum, Jharkhand)	Selection from local germplasm
28.	IC-320912	ICAR-NBPGR, New Delhi (Birra/Patamda, East Singhbhum, Jharkhand)	Selection from local germplasm
29.	IC-320913	ICAR-NBPGR, New Delhi (Goelkera/Manoharpur, West Singhbhum, Jharkhand)	Selection from local germplasm
30.	IC-320969	ICAR-NBPGR, New Delhi (ChaitiRahar, Palamau, Jharkhand)	Selection from local germplasm
31.	IC-341238	ICAR-NBPGR, New Delhi (Kumbhari (Bhakarohan), Jalna, Maharashtra)	Hogla Variety

32.	IC-341242	ICAR-NBPGR, New Delhi (Latifpur, Jalna, Maharashtra)	Selection from local germplasm
33.	IC-341248	ICAR-NBPGR, New Delhi (Pimpri, Aurangabad, Maharashtra)	Selection from local germplasm
34.	IC-341271	ICAR-NBPGR, New Delhi (Ambala, Aurangabad, Maharashtra)	Selection from local germplasm Kulith
35.	IC-341278	ICAR-NBPGR, New Delhi (Ambala, Aurangabad, Maharashtra)	Selection from local germplasm Kulith
36.	IC-341302	ICAR-NBPGR, New Delhi (Khatkhed, Aurangabad, Maharashtra)	Selection from local germplasm Kulith
37.	IC-343105	ICAR-NBPGR, New Delhi (Ghosla, Aurangabad, Maharashtra)	Selection from local germplasm Ral
38.	IC-342685	ICAR-NBPGR, New Delhi (Dorma/Torpa, Khunti, Jharkhand)	Selection from local germplasm
39.	IC-342971	ICAR-NBPGR, New Delhi (Raidih/Palkot, Gumla, Jharkhand)	Selection from local germplasm
40.	IC-342973	ICAR-NBPGR, New Delhi (Bhadosukra/Bokaro, Bokaro, Jharkhand)	Selection from local germplasm
41.	IC-342974	ICAR-NBPGR, New Delhi (Kasmar/Peterwar, Bokaro, Jharkhand)	Selection from local germplasm
42.	IC-344193	ICAR-NBPGR, New Delhi (Asurde, Ratnagiri, Maharashtra)	Selection from local germplasm
43.	IC-347175	ICAR-NBPGR, New Delhi (Sipur/Barahat, Bhagalpur, Bihar)	Selection from local germplasm
44.	IC-347180	ICAR-NBPGR, New Delhi (Bariyarpur/Bariyarpar, Munger, Bihar)	Selection from local germplasm
45.	IC-347181	ICAR-NBPGR, New Delhi (Lakratand/Dumka, Dumka, Jharkhand)	Selection from local germplasm
46.	IC-347450	ICAR-NBPGR, New Delhi (Subbam pet, Khammam, Telangana)	Selection from local germplasm
47.	IC-347593	ICAR-NBPGR, New Delhi (Bethagollagudem, Khammam, Telangana)	Selection from local germplasm
48.	IC-347894	ICAR-NBPGR, New Delhi (Chaibasa, West, Singhbhum, Jharkhand)	Selection from local germplasm
49.	IC-395656	ICAR-NBPGR, New Delhi (Himachal Pradesh)	Selection from local germplasm
50.	IC 345450	ICAR-NBPGR, New Delhi (Dongarsawan, Gadchiroli, Maharashtra)	Selection from local germplasm

traits revealed highly significant differences, indicating the existence of substantial genetic variability, which provides a strong base for crop improvement. Such variability forms the basis for effective selection and further crop improvement. Seed yield showed the widest range of variation as reflected by its high genotypic and phenotypic coefficients of variation, along with high heritability and genetic advance as a percentage of mean, indicating considerable genetic diversity for this trait within the population.

Among the yield-related traits, the number of pods per plant displayed pronounced variability, supported by high heritability and genetic advance estimates, suggesting that this trait is strongly influenced by genetic factors and may respond well to selection. Plant height and 1000-seed weight exhibited moderate variability; however, both traits recorded high heritability and appreciable genetic advance, implying that their expression is largely governed by additive genetic effects. The number of seeds per pod also showed moderate genetic variability combined with high heritability, indicating the potential for measurable improvement through selection.

The phenological traits, days to 50% flowering and days to maturity, showed very high heritability coupled with relatively narrow variability, suggesting that although these traits are under strong genetic control, the available variation for selection is limited. In contrast, the number

Table 2. Analysis of Variance treatment adjusted

Source	DF	Mean. Sq							
		NPB	PH	DF	NPP	NSP	DM	1000 SW	SY
Block (ignoring treatments)	2	0.10^{ns}	287.61*	129.33**	793.73**	1.04**	776.18**	54.33**	61550.21^{ns}
Treatment (eliminating blocks)	55	0.55**	929.55**	179.34**	301.57**	0.53**	568.96**	53.71**	97206.36**
Treatment: Check	5	1.37**	2690.50**	500.90**	1243.21**	1.77**	1400.89**	264.41**	62512.27*
Treatment: Test and Test vs. Check	50	0.46**	753.46**	147.18**	207.41**	0.41**	485.76**	32.64**	100675.77**
Residuals	10	0.04	53.00	1.17	26.40	0.06	3.59	1.11	18352.93

$^{ns}p >0.05$, $^{*}p <=0.05$, $^{**}p <=0.01$

Table 3. Analysis of Variance block adjusted

Source	DF	Mean. Sq							
		NPB	PH	DF	NPP	NSP	DM	1000 SW	SY
Treatment (ignoring blocks)	55	0.55**	939.37**	184.00**	329.39**	0.57**	597.00**	55.57**	98733.55**
Treatment: Check	5	1.37**	2690.50**	500.90**	1243.21**	1.77**	1400.89**	264.41**	62512.27*
Treatment: Test	49	0.19**	217.52**	32.95**	206.71**	0.46**	166.20**	22.24**	85583.92**
Treatment: Test vs. Check	1	14.10**	27554.21**	6000.96**	1771.54**	0.04^{ns}	17686.44**	644.91**	924171.63**
Block (eliminating treatments)	2	0.02^{ns}	17.68^{ns}	1.17^{ns}	28.61^{ns}	0.01^{ns}	5.06^{ns}	2.94^{ns}	19552.67^{ns}
Residuals	10	0.04	53.00	1.17	26.40	0.06	3.59	1.11	18352.93

$^{ns}P>0.05$, $^{*}p <=0.05$, $^{**}p <=0.01$

Degree of freedom=DF, Number of primary branches=NPB, Plant height (cm)= PH, Days to 50% flowering=DFF, Number of pods per plant=NPP, Number of seeds per pod=NSP, Days to Maturity=DM, 1000 Seed weight (g)=1000 SW and Seed yield (kg/ha) =SW

of primary branches per plant recorded low variability and low genetic advance, despite moderate heritability, indicating restricted opportunities for genetic enhancement of this trait through direct selection. Overall, the variability parameters presented in Table 4 highlight a diverse genetic base, particularly for yield and pod-related traits, which may be valuable for future breeding efforts.

Correlation

The correlation analysis among the quantitative traits of horse gram genotypes showed several significant associations influencing seed yield, as summarized in Table 5 and illustrated in Fig. 1. Seed yield exhibited strong positive associations with key reproductive traits, particularly the number of pods per plant, followed by the number of seeds per pod and phenological traits such as days to 50% flowering and days to maturity. These trends indicate that genotypes producing more pods and seeds generally tend to achieve higher yields.

The number of pods per plant, a major yield-determining component, showed strong positive correlations with plant height, days to flowering, days to maturity and number of seeds per pod. This interrelationship reflects the combined influence of vegetative vigour and extended reproductive duration on pod production. The moderate and significant correlations between plant height and phenological traits, *viz.,* days to flowering and days to maturity, further suggest that taller genotypes generally possess longer growth cycles, which may favour yield accumulation but could reduce suitability under terminal moisture stress.

A weak but positive correlation was observed between plant height and seed yield, indicating that moderate plant stature contributes to yield without excessive biomass allocation. In contrast, 1000-seed weight exhibited a

Table 4. Estimation of overall adjusted mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as a percent of mean for quantitative characters in horse gram genotypes

S. No.	Characters	Overall adjusted mean	GCV	PCV	Heritability (Broad Sense)	Genetic advance	Genetic advance as % of mean
1	No. of primary branches	4.47	8.56	9.68	78.05	0.69	15.60
2	Plant height	93.41	13.73	15.78	75.63	23.01	24.63
3	Days to flowering	65.18	8.64	8.80	96.45	11.42	17.52
4	No. of pods/plant	42.14	31.86	34.11	87.22	25.87	61.39
5	No. of seeds/pod	5.04	12.57	13.44	87.53	1.22	24.27
6	Days to maturity	125.09	10.19	10.30	97.84	26.02	20.80
7	1000 seed weight (g)	36.49	12.59	12.92	95.02	9.24	25.33
8	Yield (kg/ha)	608.12	42.63	48.10	78.55	474.10	77.96

Table 5. Matrix of correlation coefficients of the quantitative characters of horse gram

	Number of primary branches	Plant height (cm)	Days to flowering	Number of pods/plant	Number of seeds/ pods	Days to maturity	1000 seed weight (g)	Yield (kg/ha)
Number of primary branches	**1**	-0.166	-0.223	0.062	0.203	-0.163	0.209	0.222
Plant height (cm)	-0.166	**1**	0.326*	0.4**	-0.042	0.395**	-0.31*	0.21
Days to flowering	-0.223	0.326*	**1**	0.412**	0.161	0.927***	-0.198	0.395**
Number of pods per plant	0.062	0.4**	0.412**	**1**	0.425**	0.492***	-0.161	0.64***
Number of seeds per pod	0.203	-0.042	0.161	0.425**	**1**	0.135	0.381**	0.437**
Days to maturity	-0.163	0.395**	0.927***	0.492***	0.135	**1**	-0.317*	0.38**
1000 seed weight (g)	0.209	-0.31*	-0.198	-0.161	0.381**	-0.317*	**1**	0.104
Yield (kg/ha)	0.222	0.21	0.395**	0.64***	0.437**	0.38**	0.104	**1**

negative correlation with plant height and days to maturity, suggesting a reciprocal relationship between seed size and vegetative growth or crop duration, which is an important consideration when targeting short-duration or resource-limited environments.

The number of primary branches exhibited negative associations with flowering and maturity, suggesting that early-maturing genotypes have limited branching due to a shorter vegetative phase. Although branching showed only a weak association with yield, the overall pattern highlighted the importance of emphasizing reproductive attributes, particularly pod number, seeds per pod, and moderate-to-extended maturity, while selecting for high-yielding genotypes.

Principal Component Analysis (PCA)

Principal component analysis (PCA) of eight quantitative traits in horse gram genotypes (Fig. 2) revealed that the first four principal components together accounted for 83.35% of the total variability, indicating that a large proportion of the genetic diversity among genotypes can be effectively captured using these components. Among these, PC1

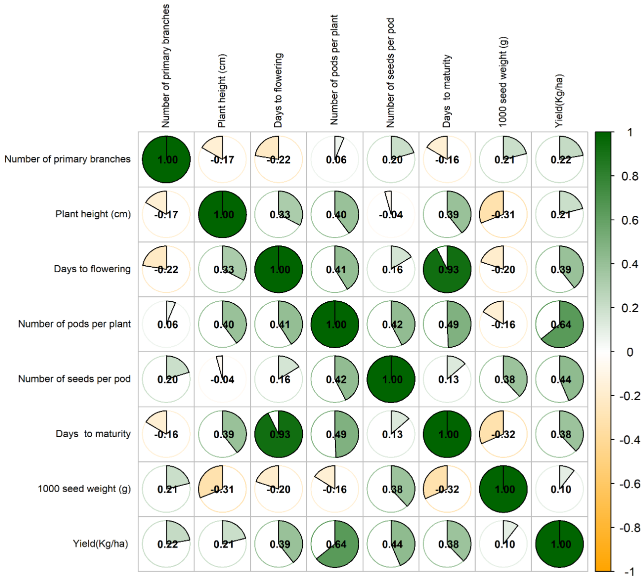

Fig. 1. Pictorial representation of the correlation matrix of quantitative characters in horsegram

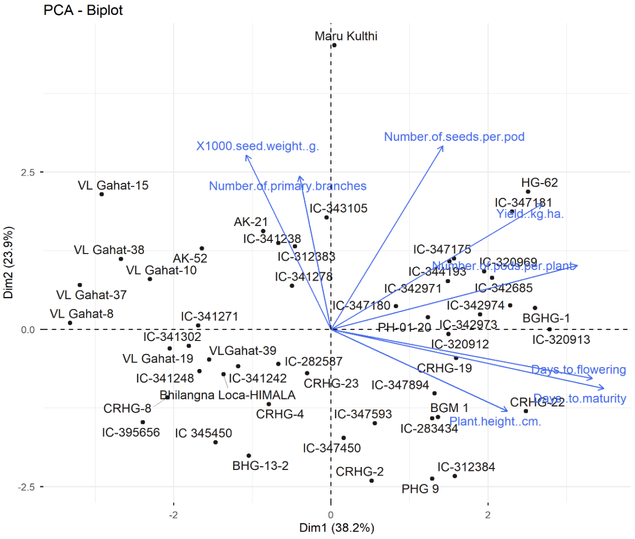

Fig. 2. Biplot of factor coordinates for PC1 and PC2 of the quantitative characters in horsegram

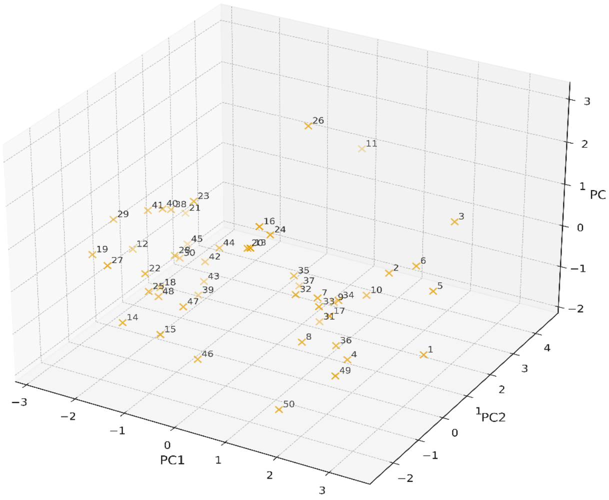

Fig. 3. Three-dimensional principal component analysis (PCA) of genetic diversity in horsegram genotypes

had the highest eigenvalue (3.056), contributing 38.20% of the variation, and thus represents the most dominant axis of variability, as detailed in Table 6. PC2 accounted for 23.88% (eigenvalue: 1.911), followed by PC3 and PC4, which explained 11.86 and 9.40%, respectively. In terms of trait contributions, PC1 was largely influenced by days to maturity (0.498), days to flowering (0.477), number of pods per plant (0.450), and yield per plant (0.386), indicating a focus on phenological and yield-related characteristics. Genotypes with higher PC1 scores are therefore likely to be late-maturing but high-yielding. Three-dimensional (3D) PCA pictorial representation of genetic diversity in horsegram genotypes is shown in Fig. 3.

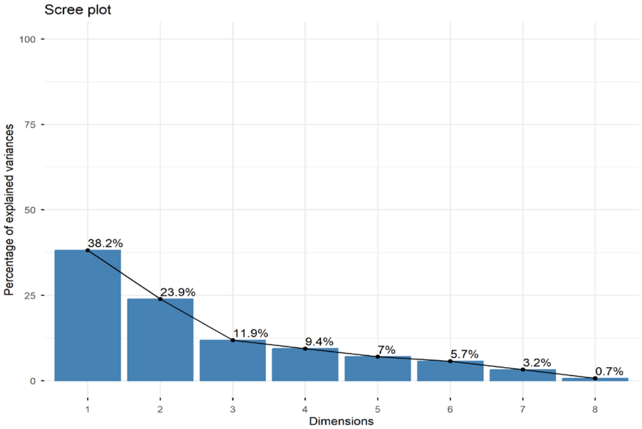

Fig. 4. Scree plot representing the variation in the principal components

PC2 captured seed and branching pattern traits, with high positive contributions from number of seeds per pod (0.530), 1000 seed weight (0.503), and number of primary branches (0.443). PC3emphasized vegetative growth components, particularly the number of primary branches (0.526) and plant height (0.407), indicating its relevance in identifying genotypes with a resilient plant type. In contrast, PC4 presented a mixture of both favourable and unfavourable trait contributions. Positive loadings were observed for the number of primary branches (0.601) and days to maturity (0.334), whereas plant height (-0.515) and 1000 seed weight (-0.223) showed negative loadings. This suggests a potential contradiction between vegetative growth and seed development traits.

A steep decline in eigenvalues from PC1 to PC2 indicates that the initial principal components capture the majority of the variation, as depicted in the scree plot (Fig. 4). Specifically, PC1 accounts for 38.20% of the total variance, followed by PC2 (23.88%), PC3 (11.86%), and PC4 (9.40%). The cumulative variance explained by these four components is around 83.34%, reaffirming their critical role in explaining genotypic variation.

Discussion

The observed variability among the genotypes confirmed the existence of a broad genetic base for most quantitative traits in horse gram, providing ample scope for selection and genetic improvement. The presence of highly significant differences for all traits indicates substantial inherent diversity within the evaluated germplasm. Seed yield (kg/ha) and number of pods per plant exhibited high genotypic and phenotypic coefficients of variation along with high heritability and high genetic advance as a percentage of mean (GAM). High heritability coupled with high GAM suggests the predominance of additive gene action, implying that these traits are amenable to direct selection. Therefore, both seed yield and number of pods per plant can be effectively improved through simple phenotypic

Table 6. Eigenvalue, factor scores and contribution of the principal component axes to variation in horsegram

Particulars	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigen value	3.056	1.911	0.949	0.752	0.563	0.456	0.259	0.055
Percentage of variance	38.203	23.883	11.861	9.40	7.032	5.696	3.238	0.687
Cumulative percentage of variance	38.203	62.086	73.947	83.347	90.378	96.075	99.313	100
No. of primary branches	-0.058	0.443	0.526	0.601	-0.306	0.245	-0.063	0.073
Plant height (cm)	0.322	-0.236	0.407	-0.515	-0.595	0.181	0.149	0.024
Days to flowering	0.477	-0.141	-0.396	0.31	-0.185	0.027	0.015	0.682
No. of pods/plant	0.45	0.185	0.282	-0.219	0.368	-0.048	-0.698	0.103
Number of seeds/pod	0.204	0.53	-0.225	-0.261	0.246	0.614	0.348	-0.01
Days to maturity	0.498	-0.17	-0.238	0.334	-0.129	0.137	-0.108	-0.712
1000 seed weight	-0.155	0.503	-0.438	-0.223	-0.548	-0.215	-0.359	-0.074
Yield (kg/ha)	0.386	0.363	0.149	0.009	0.067	-0.68	0.473	-0.078

selection. Similar conclusions were drawn by Vijayakumar et al. (2016), Neelima et al. (2021), and Bhavsar et al. (2021), who also reported high heritability and genetic advance for these yield-related traits in horse gram.

Traits such as 1000-seed weight, number of seeds per pod, and plant height displayed moderate GCV values but high heritability with moderate GAM. This indicates that these traits are under both additive and non-additive gene effects, and while improvement through selection is feasible, the expected gain may be moderate. Hence, these traits can be improved indirectly, either through correlated selection with seed yield or by incorporating them into a multi-trait selection index. The present findings are consistent with those of Ramesh et al. (2020), while Karthik et al. (2023) observed slightly higher variability for seed weight, likely due to differences in the genetic background of the studied material and environmental conditions.

Maturity traits such as days to 50% flowering and days to maturity recorded very high heritability but low GCV and GAM, reflecting a narrow genetic base and suggesting the predominance of non-additive gene effects. This indicates that improvement through direct selection would be limited, and these traits may instead be targeted for indirect improvement through hybridization or by introgressing diverse parental lines to enhance variability. Similar results were reported by Vijayakumar et al. (2016) and Priyanka et al. (2021b). The number of primary branches per plant exhibited low GCV and PCV values, moderately high heritability, and low GAM, indicating restricted potential for genetic gain through direct selection due to limited genetic variability and environmental influence. Such traits may require indirect improvement through recombination breeding, introduction of exotic germplasm, or mutagenesis to widen their genetic base.

Therefore, seed yield and number of pods per plant are the most promising traits for direct selection owing to their high heritability and high GAM, indicative of additive gene action. In contrast, 1000-seed weight, number of seeds per pod, and plant height may respond better to indirect selection strategies. Meanwhile, maturity and branching traits with high heritability but low variability would benefit from genetic diversification approaches such as hybridization or mutagenic enhancement to create new variability and improve their selection response.

Correlation analysis provides valuable insights into the interrelationships among yield and its component traits, thereby guiding the formulation of effective selection strategies in crop improvement. In the present study, seed yield exhibited strong and positive associations with the number of pods per plant, number of seeds per pod, days to flowering, and days to maturity, suggesting that these traits play decisive roles in determining productivity in horse gram. The strongest association between seed yield and number of pods per plant indicates that pod number is the most direct and reliable determinant of yield potential. Similar findings have been reported by Ragini et al. (2025), Sidar *et al.* (2024), Swathy *et al.* (2022), and Kumari (2023), who identified pod number as a dependable selection index in legume breeding programs.

The positive correlation between seed yield and number of seeds per pod underscores the importance of reproductive efficiency in enhancing yield. This observation aligns with the findings of Swathy *et al.* (2022), who noted that an increase in seed number contributes additively to total yield. Likewise, the positive associations of yield with days to flowering and days to maturity imply that genotypes with extended vegetative and reproductive durations accumulate assimilates for a longer period, resulting in improved yield formation. This supports the earlier findings in horse gram of Swathy et al. (2019) and contrasting results were documented by Alle et al. (2016). However, such relationships must be interpreted with caution in the context of production environments. Under favourable or irrigated conditions, a longer duration can indeed enhance productivity by supporting greater biomass accumulation and seed development. Conversely, in rainfed or drought-prone regions where terminal moisture stress is common, prolonged maturity may expose the crop to adverse climatic conditions, leading to yield reduction. This indicates that while extended duration contributes positively to yield under optimal conditions, breeding programs targeting marginal environments should aim for genotypes that balance duration and productivity to ensure adaptability and yield stability.

The number of pods per plant, besides its direct correlation with yield, showed strong positive associations with plant height, days to flowering, and days to maturity. This suggests that taller and moderately late-maturing genotypes tend to produce more pods due to enhanced photosynthetic capacity and assimilate partitioning toward reproductive structures. Similar trends were reported by Sidar et al. (2024). Although 1000-seed weight was negatively associated with plant height and days to maturity, indicating an inverse relationship between seed size and growth duration. This suggests a compensatory mechanism wherein genotypes allocating more resources to prolonged vegetative or reproductive phases tend to produce smaller seeds. Such negative associations are commonly reported in pulses and highlight the difficulty of improving seed size and yield simultaneously through simple selection.

Overall, the correlation analysis indicates that pod number per plant, seed number per pod, and maturity duration are the most influential traits contributing to yield formation in horse gram. Nevertheless, breeding strategies should carefully consider the production environment, particularly rainfall pattern, growing season length, and terminal stress occurrence when exploiting these relationships. Selection for high pod number and moderate maturity duration may be most beneficial for improving yield under rainfed and resource-constrained conditions, while longer duration, high-biomass genotypes may be better suited to favourable environments.

Principal Component Analysis (PCA) is a powerful multivariate tool for understanding the relative contribution of yield and associated traits to overall genetic variability. In the present study, the first four PCs accounted for 83.35% of the total variation, indicating that a few principal components are sufficient to explain most of the diversity among horse gram genotypes. Similar high cumulative variance (>80%) explained by initial PCs has been reported in horse gram (Bhardwaj et al. 2012) and other legumes (Arora et al. 2021), reinforcing the efficiency of PCA in dimensionality reduction and genotype classification.

PC1, which explained the maximum variance (38.20%), was mainly influenced by days to maturity, days to flowering, pods per plant, and seed yield, suggesting that maturity and yield-related traits are the most dominant sources of variability. Genotypes scoring high on PC1 are therefore characterized by longer reproductive duration and higher productivity. These findings agree with Singh et al. (2018), who reported that the first component in legumes typically loads heavily on maturity and yield attributes. In contrast, Kumar and Singh (2015) in moth bean observed that seed yield was not strongly represented in early PCs, highlighting possible crop-specific differences in trait expression.

PC2 (23.88%) was associated with the number of seeds per pod, 1000-seed weight, and number of primary branches, indicating its role in capturing variation related to seed and branching traits. Comparable results were reported by Sharma et al. (2020) in black gram, where PC2 emphasized seed size and branching patterns. PC3 was dominated by primary branches and plant height, reflecting vegetative growth components, while PC4 revealed contrasting contributions, with positive loadings for branches and maturity but negative loadings for plant height and seed weight. This suggests a potential negative relation between vegetative vigour and seed development.

The scree plot further confirmed that the first four PCs capture the majority of the variation, with a steep decline in eigenvalues beyond PC2. This pattern is consistent with Arora et al. (2021), who suggested that three to four PCs are adequate for genotype differentiation in legumes. Overall, the PCA results highlight that PC1 and PC2 are the most informative, jointly explaining over 62% of the variability, and are effective in differentiating genotypes based on yield, maturity, seed size, and branching. These components provide critical insights for identifying superior genotypes and selecting diverse parents in horse gram breeding programs aimed at yield enhancement and genetic improvement.

Authors' contribution

Conceptualization of research (MN, RC, RB); Designing of the experiments (MN, R, RB) Contribution of experimental materials (MN, RC, RB); Execution of field/lab experiments and data collection (MN, R, RB); Analysis of data and interpretation (MN, R, RB, DSJ, PK); Preparation of the manuscript (MN, RC, DSJ, PK, BLK).

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